

1 TCAAATTTTT CTCCAGTTCT AAATATCCGG AACCTCTTG GGATGCCATT
51 GCCCATCTAT CTGTAATTTA TTGACGAAAT AGACGAAAAG GAAGGTGGCT
101 CCTATAAAGC ACATCATTGC GATAACAGAA AGGCCATTGT TGAAGATACC
151 TCTGCTGACA TTGGTCCCCA AGTGGAAGCA CCACCCCATG AGGAGCACCG
201 TGGAGTAAGA AGACGTTCTGA GCCACGTCGA AAAAGCAAGT GTGTTGATGT
251 AGTATCTCCA TTGACGTAAG GGATGACGCA CAATCCAAC TATCCATCGCA
301 AGACCATTGC TCTATATAAG AAAGTTAATA TCATTTTCGAG TGGCCACGCT
351 G [SEQ ID NO:2]

FIGURE 2